

-continued

```

<210> SEQ ID NO 13
<211> LENGTH: 50
<212> TYPE: RNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: aptamer

<400> SEQUENCE: 13

uugggguggg guggggaaag uccuuaaaag agggccacca cagaagcaau      50

<210> SEQ ID NO 14
<211> LENGTH: 86
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: aptamer

<400> SEQUENCE: 14

gggagcttct ggactgcgat gggagcacga aacgtcgtgg cgcaattggg tggggaaagt      60
ccttaaaaga gggccaccac agaagc                                     86

<210> SEQ ID NO 15
<211> LENGTH: 120
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: aptamer

<400> SEQUENCE: 15

gggaatggat ccacatctac gaattcccaa cgactgccga gcgagattac gcttgagcgc      60
cccactgagg atgccacgg gcgattgggg cacggcttca ctgcagactt gacgaagctt      120

```

What is claimed:

1. A method for analyzing a molecular target in a sample, said method comprising:

providing an aptamer, wherein said aptamer is a high affinity binding partner to at least a portion of the molecular target in the sample;

contacting said aptamer with said sample containing the molecular target under conditions effective for the molecular target and aptamer to bind to each other;

separating the molecular target from the sample to form a molecular target enriched sample; and

analyzing the separated molecular target of the enriched sample.

2. The method of claim 1, wherein said analyzing comprises a method selected from mass spectrometry, cryo-electron microscopy, and nucleotide sequencing.

3. The method of claim 1, wherein the molecular target comprises one or more biomolecules.

4. The method of claim 3, wherein the one or more biomolecules is selected from a protein, polypeptide, peptide, ribonucleic acid (RNA), deoxyribonucleic acid (DNA), lipid, carbohydrate, and any combination thereof.

5. The method of claim 1, further comprising:

providing, after said separating, a binding agent that binds to a different portion of the molecular target than bound by the aptamer;

contacting the molecular target enriched sample with the binding agent under conditions effective for the molecular target and binding agent to bind to each other;

immunoprecipitating the binding agent to isolate the molecular target from the enriched sample, whereby said isolated molecular target is subjected to said analyzing.

6. The method of claim 5, wherein the binding agent is an antibody or binding fragment thereof.

7. The method of claim 1, wherein the sample is cross-linked prior to said contacting with said aptamer.

8. The method of claim 1, further comprising:

providing a binding agent that binds to a different portion of the second molecular target than bound by the aptamer;

introducing the binding agent into the sample, prior to said contacting with said aptamer, under conditions effective for the molecular target and binding agent to bind to each other;

immunoprecipitating the binding agent to isolate the molecular target from the sample, whereby said isolated molecular target is subjected to said contacting with said aptamer.

9. The method of claim 8, wherein said sample is cross-linked prior to introducing the binding agent.

10. The method of any one of claim 8, wherein the binding agent is an antibody or binding fragment thereof.